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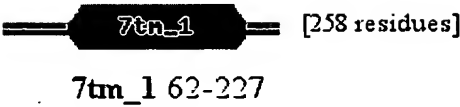
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FIGURE 1A

Domain	Start	End	Bits	Evalue	Alignment
7tm_1	62	227	142.90	2.6e-44	Align



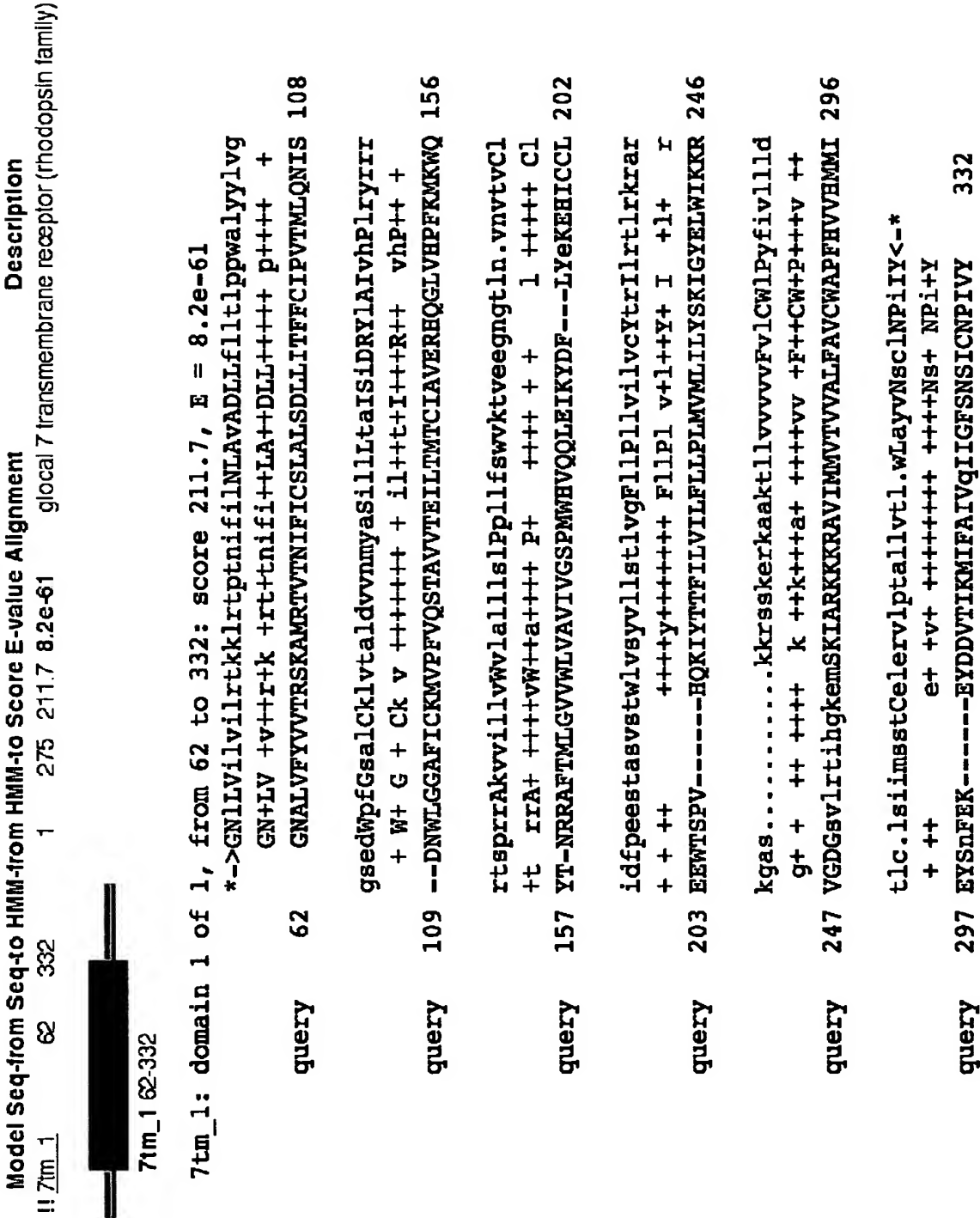
Alignments of Pfam-A domains to HMMs

Format for fetching alignments to seed [Hypertext linked to swisspfam](#)

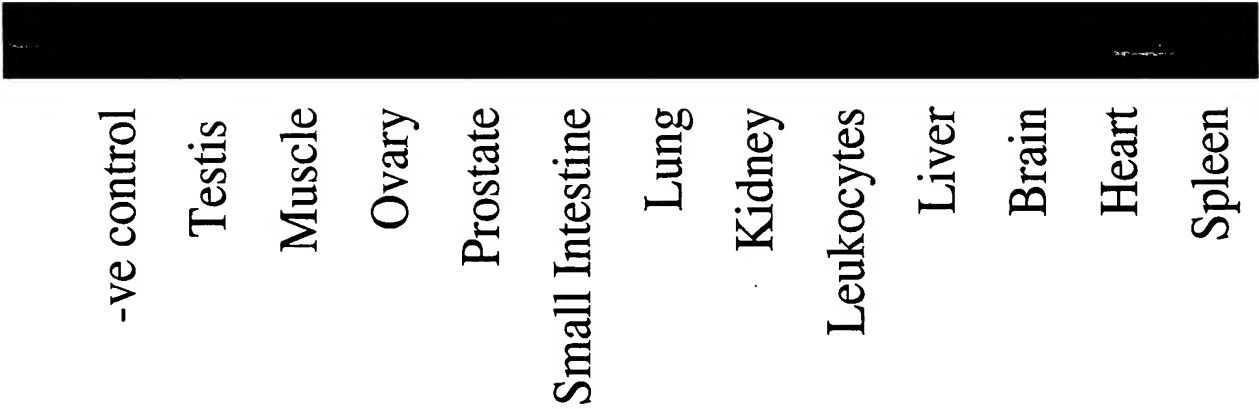
Alignment of 7tm\_1 vs UserSeq/62-227

		*->GNILVilvilrtkkrlrtptnifiNLAvADLLflltlppwalyylv	
		GN+LV +v++r+k +rt+tnifi++LA++DLL+++++ p++++ +	
UserSeq	62	GNALVFYVTRSKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNIS	108
		gsedWpfGsalCklvtaldvvnmyaSi11LtaISiDRYlAIVhPlryrrr	
		+ W+ G + Ck v ++++++ + il++t+I++R++ vHP++ +	
UserSeq	109	--DNWLGGAFICKMVPFVQSTAVVTEILTMTCIAVERHQGLVHPFKMKWQ	156
		rtsprrrAkvvillvWvlalllslPp11fswvktveegngtln.vnvtvCl	
		+t rrA+ +++vW++a++++ P+ +++++ + + 1 +++++ Cl	
UserSeq	157	YT-NRRAFTMLGVVWLVAVIVGSPMWHVQOLEIKYDF---LYeKEHICCL	202
		idfpeestasvstwlrsyvllstlvGFllPl<-*	
		+ + ++ +++++y+++++++ FllPl	
UserSeq	203	EEWTSPV-----HQKIYTTFILVILFLLPL	227

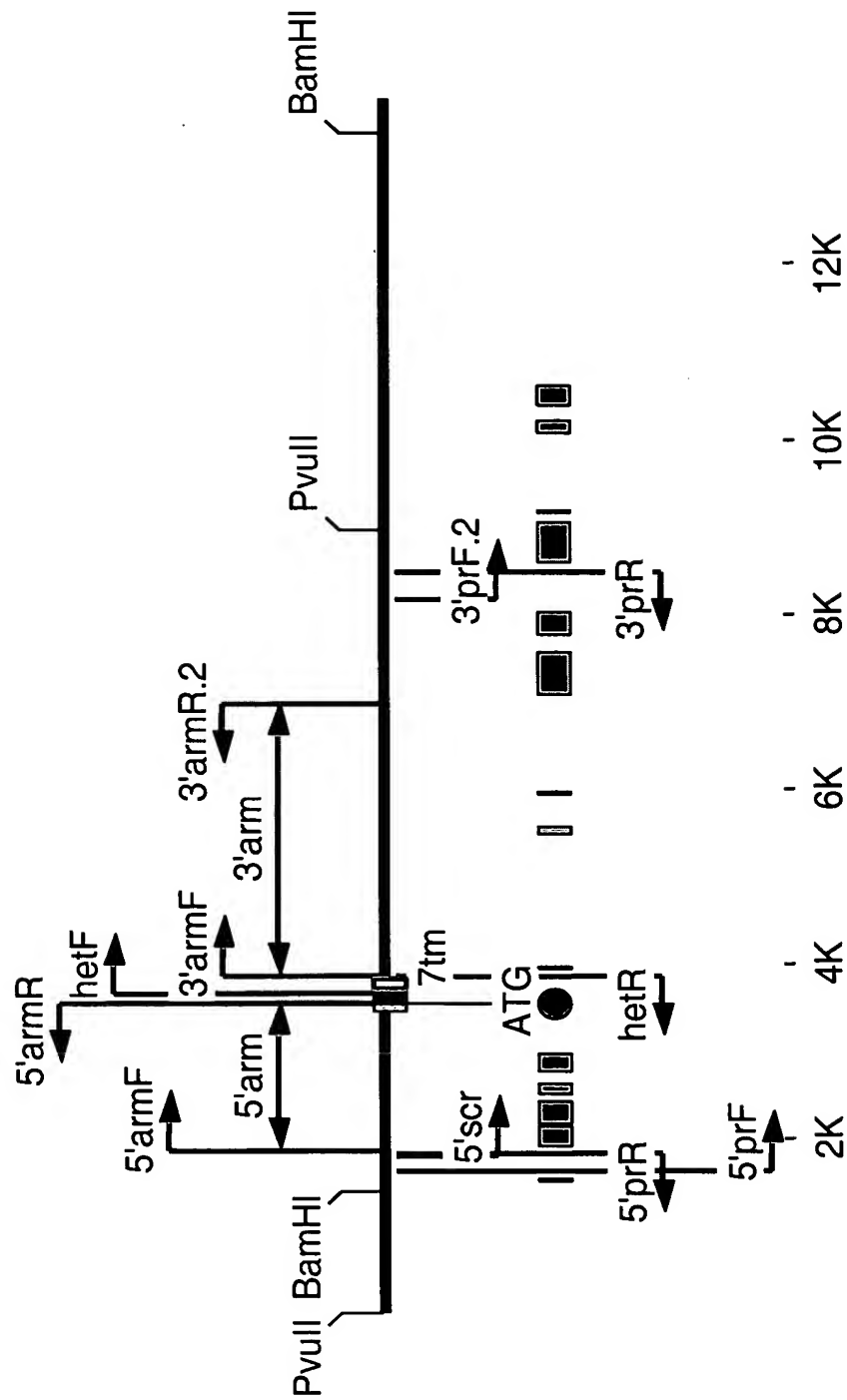
FIGURE 1B



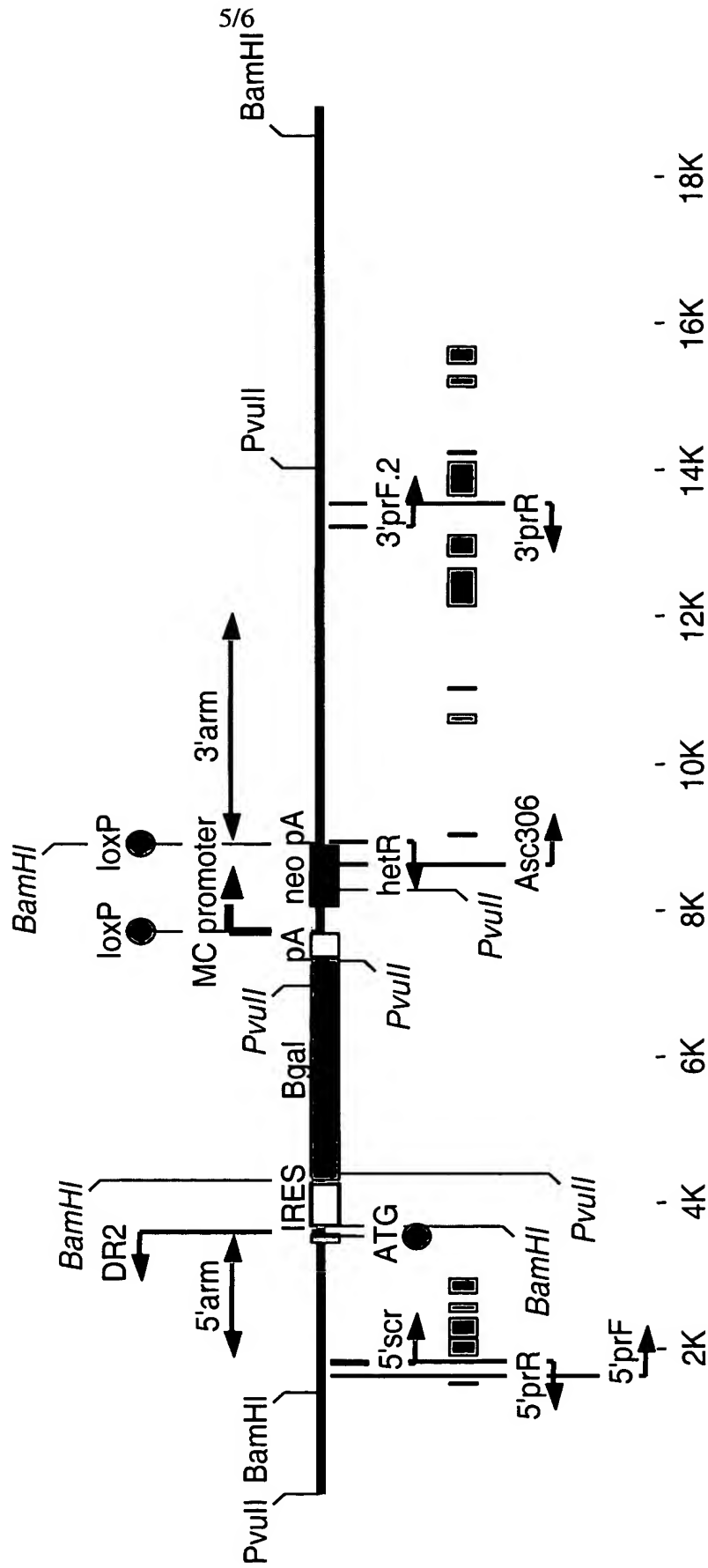
**FIGURE 2**



**FIGURE 3**



**FIGURE 4**



**FIGURE 5**

